



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/712,715
Source: FWO
Date Processed by STIC: 7/23/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/7/2/715

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (Sec "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/712,715

DATE: 07/23/2004

TIME: 11:04:28

Input Set : A:\14683Z.seq.txt

Output Set: N:\CRF4\07232004\J712715.raw

3 <110> APPLICANT: SUYAMA, AKIRA
 4 HORI, KUNIO
 6 <120> TITLE OF INVENTION: METHOD OF DETECTING NUCLEIC ACID
 8 <130> FILE REFERENCE: 14683Z
 10 <140> CURRENT APPLICATION NUMBER: US 10/712,715
 11 <141> CURRENT FILING DATE: 2003-11-13
 13 <160> NUMBER OF SEQ ID NOS: 16
 15 <170> SOFTWARE: PatentIn version 3.2
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 16
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Probe ← Invalid Response
 22 <400> SEQUENCE: 1
 23 ctagtaggggt gaagtc
 26 <210> SEQ ID NO: 2
 27 <211> LENGTH: 64
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Probe ← Mandatory, <213> responses has to be either artificial/unknown or genus/species.
 31 <400> SEQUENCE: 2
 32 cataagagcc ctagagcatg ctggtcaagg ggcacgcggt tcatacaggag tcgaaggcag 60
 34 gacg 64
 37 <210> SEQ ID NO: 3
 38 <211> LENGTH: 32
 39 <212> TYPE: DNA
 40 <213> ORGANISM: Probe ← same error
 42 <400> SEQUENCE: 3
 43 ctctagggct cttatggact tcaccctact ag 32
 46 <210> SEQ ID NO: 4
 47 <211> LENGTH: 48
 48 <212> TYPE: DNA
 49 <213> ORGANISM: Probe ← same error
 51 <400> SEQUENCE: 4
 52 cgtcctgect tcgactcctg atgaaccgcy tgccccttga ccagcatg 48
 55 <210> SEQ ID NO: 5
 56 <211> LENGTH: 32
 57 <212> TYPE: DNA
 58 <213> ORGANISM: Probe ← same error
 60 <400> SEQUENCE: 5
 61 ttctagagct cctatggact tcgccctact ag 32
 64 <210> SEQ ID NO: 6
 65 <211> LENGTH: 30
 66 <212> TYPE: DNA
 67 <213> ORGANISM: Mouse

↑ pls see item # 10
 on error summary sheet.

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69 <400> SEQUENCE: 6
70 tcctatatattc aactgtaata gcccgttcct 30
73 <210> SEQ ID NO: 7
74 <211> LENGTH: 30
75 <212> TYPE: DNA
76 <213> ORGANISM: Mouse
78 <400> SEQUENCE: 7
79 attttcctct gaaacaataa agtcggttcc 30
82 <210> SEQ ID NO: 8
83 <211> LENGTH: 15
84 <212> TYPE: DNA
85 <213> ORGANISM: Probe
87 <400> SEQUENCE: 8
88 tcctatatattc aactg 15
91 <210> SEQ ID NO: 9
92 <211> LENGTH: 15
93 <212> TYPE: DNA
94 <213> ORGANISM: Probe
96 <400> SEQUENCE: 9
97 attttcctct gaaac 15
100 <210> SEQ ID NO: 10
101 <211> LENGTH: 15
102 <212> TYPE: DNA
103 <213> ORGANISM: Probe
105 <400> SEQUENCE: 10
106 taatagcccg ttctt 15
109 <210> SEQ ID NO: 11
110 <211> LENGTH: 15
111 <212> TYPE: DNA
112 <213> ORGANISM: Probe
114 <400> SEQUENCE: 11
115 aataaagtcg gttcc 15
118 <210> SEQ ID NO: 12
119 <211> LENGTH: 25
120 <212> TYPE: DNA
121 <213> ORGANISM: Probe
123 <400> SEQUENCE: 12
124 tgaagtcacc acaacacaca gtaca 25
127 <210> SEQ ID NO: 13
128 <211> LENGTH: 25
129 <212> TYPE: DNA
130 <213> ORGANISM: Probe
132 <400> SEQUENCE: 13
133 tctcagtcctc agtccatttc cttac 25
136 <210> SEQ ID NO: 14
137 <211> LENGTH: 25
138 <212> TYPE: DNA
139 <213> ORGANISM: Probe
141 <400> SEQUENCE: 14

Same error

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Input Set : A:\14683Z.seq.txt

Output Set: N:\CRF4\07232004\J712715.raw

142 acgacgatga aaaactacga gggac 25
145 <210> SEQ ID NO: 15
146 <211> LENGTH: 25
147 <212> TYPE: DNA
148 <213> ORGANISM: (Probe) - SAME ERROR
150 <400> SEQUENCE: 15
151 tgaacccccca agtttagatc tcagc 25
154 <210> SEQ ID NO: 16
155 <211> LENGTH: 25
156 <212> TYPE: DNA
157 <213> ORGANISM: (Probe) - SAME ERROR
159 <400> SEQUENCE: 16
160 gacaaacacc ccgaatacaa acagc 25

VERIFICATION SUMMARY

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